This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-16. (Canceled)

17. (New) A method of sequencing in parallel at least one nucleotide of a plurality of polynucleotide sample fragments, the method comprising:

(a) providing a plurality of polynucleotide sample fragments,

(b) from said sample fragments, forming a mixture of sequencing fragments, wherein (1) each sequencing fragment terminates at a predefined end with a known base, and (2) each sequencing fragment contains an identifier tag sequence which identifies the sample fragment to which the sequencing fragment corresponds and optionally, the terminating base-type of the fragment, wherein said forming includes the steps of:

(1) hybridizing to each sample fragment, a tagged primer containing (i) an identifier tag sequence, and (ii) a primer sequence located on the 3'-side of the tag sequence wherein each tagged primer has a primer sequence that is complementary to a unique sample fragment in said plurality of sample fragments, to form a plurality of tagged primer-sample fragment hybrids, where at least one different identifier tag sequence is used to identify each sample fragment,

(2) performing a chain extension reaction on each hybrid to form sequencing fragments extended by at least one base, and

(3) combining the sequencing fragments generated from the hybrids, to form a sequencing fragment mixture,

(c) contacting the sequencing fragment mixture with an array of immobilized different-sequence tag probes, each tag probe (1) being capable of hybridizing specifically with one of said identifier tag sequences, and (2) having an addressable location in said array, where said contacting is conducted under conditions effective to provide specific hybridization of the

identifier tag sequences, or tag sequence complements, with the corresponding immobilized tag probes, to form a hybridization pattern on said array, and

(d) from the hybridization pattern formed, determining a nucleotide sequence for at least one base in at least one sample fragment.

18. (New) The method of claim **17**, wherein for each sample fragment to be sequenced there are at least two unique tagged primers, wherein each of the tagged primers has a different tag sequence and a common primer sequence.

19. (New) The method of claim **17**, wherein for each sample fragment to be sequenced there are four unique tagged primers, wherein each of the tagged primers has a different tag sequence and a common primer sequence.

20. (New) The method of claim **18**, wherein the chain extension reaction of each of the at least two unique tagged primers is done in a separate reaction.

21. (New) The method of claim **17**, wherein the chain extension reaction is performed in the presence of chain terminating nucleotides.

22. (New) The method of claim **21**, wherein the chain terminating nucleotides are dideoxynucleotides.

23. (New) The method of claim **17**, wherein sequencing fragments are labeled with a fluorescent label.

24. (New) The method of claim **23**, wherein said fluorescent label is attached to the 5'-end of a sequencing fragment.

25. (New) The method of claim **23**, wherein said fluorescent label is attached to the 3'-end of a sequencing fragment.

26. (New) The method of claim **23**, wherein a different fluorescent label is used to identify each different terminating base-type.

27. (New) The method of claim **17**, wherein sequencing fragments are labeled with a radioactive label.

28. (New) The method of claim **17**, wherein each tag primer comprises a common priming sequence located on the 5'-side of the tag sequence.

29. (New) A polynucleotide mixture comprising:

a plurality of primer-tag-primer polynucleotides each comprising a first primer sequence, an identifier tag sequence linked to the 3'-side of the first primer sequence, a second primer sequence located on the 3'-side of the tag sequence wherein each primer-tag-primer polynucleotide has a second primer sequence that is complementary to a unique sample fragment in said plurality of sample fragments and a third primer sequence linked to the 3'-side of the second primer sequence,

wherein the first primer sequences are identical to each other, the identifier tag sequence in each primer-tag-primer polynucleotides differs from the tag sequence in every other primer-tag-primer polynucleotide and the third primer sequences are identical to each other.